

P65#26 -> Genes

DNA sequence 1665 b.p. gaattcgggtccc ... caagccgaattc linear

PGO-1

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1 gaattcgggtccat ATG GCG GCT AAA GAC GTA AAA TTC GGT AAC GAC GCT CGT GTG AAA ATG CTG CGC GGC GTA AAC 77
1 M A A K D V K F G N D A R V K M L R G V N 21

78 GTA CTG GCA GAT GCA GTG AAA GTT ACC CTC GGC CCA AAA GGC CGT AAC GTA GTT CTG GAT AAA TCT TTC GGT GCA 152
22 V L A D A V K V T L G P K G R N V V L D K S F G A 46

153 CCG ACC ATC ACT AAA GAT GGT GTT TCC GTA GCA CGT GAA ATC GAA CTG GAA GAC AAG TTC GAA AAC ATG GGT CCG 227
47 P T I T K D G V S V A R E I E L E D K F E N M G A 71

228 CAG ATG GTG AAA GAA GTT GCC TCT AAA GCG AAC GAC GCT GCA GGT GAC GGT ACC ACC ACC GCA ACC GTA CTG GCT 302
72 Q M V K E V A S K A N D A A G D G T T T A T V L A 96

303 CAG TCC ATC ATC ACT GAA GGC CTG AAA GCC GTT GCT GCG GGC ATG AAC CCG ATG GAT CTG AAA CGT GGT ATC GAC 377
97 Q S I I T E G L K A V A A G M N P M D L K R G I D 121

378 AAA GCT GTC GCT GCT GCT GTT GAA GAA CTG AAA GCA CTG TCC GTA CCG TGC TCC GAC TCT AAA GCT ATT GCT CAG 452
122 K A V A A A V E E L K A L S V P C S D S K A I A Q 146

453 GTT GGT ACC ATC TCC GCT AAC TCC GAC GAA ACC GTA GGT AAA ATC GCT GAA GCG ATG GAC AAA GTC GGT AAA 527
147 V G T I S A N S D E T V G K L I A E A M D K V G K 171

528 GAA GGC GTG ATC ACC GTT GAA GAC GGT ACC GGT CTG CAG GAC GAA CTG GAC GTG GTT GAA GGT ATG CAG TTC GAC 602
172 E G V I T V E D G T G L Q D E L D V V E G M Q F D 196

603 CGT GGC TAC CTG TCT CCT TAC TTC ATC AAC AAG CCG GAA ACT GGC GCA GTA GAA TTG GAA AGC CCG TTC ATC CTG 677
197 R G Y L S P Y F I N K P E T G A V E L E S P F I L 221

678 CTG GCT GAC AAG AAA ATC TCC AAC ATC CCG GAA ATG CTG CCG GTT CTG GAA GGT GTA GCG AAA GCA GGC AAA CCG 752
222 L A D K K I S N I R E M L P V L E A V A K A G K P 246

753 CTG CTG ATC ATC GCT GAA GAT GTT GAA GGC GAA GCG CTG GCA ACT CTG GTT GTT AAC ACC ATG CCG GGT ATC GTA 827
247 L I I A E D V E G E A L A T L V V N T M R G I V 271

828 AAA GTC GCT GCG GTT AAA GCA COT GGC TTC GGC GAT CGT CGT AAA GCA ATG CTG CAG GAT ATC GCT ACC CTG ACC 902
272 K V A A V K A P G F G D R R K A M L Q D I A T L T 296

903 GGT GGT ACC GTT ATC TCT GAA GAG ATC GGT ATG GAG CTG GAA AAA GCA ACT CTG GAA GAT CTG GGC CAG GCG AAA 977
297 G G T V I S E E I G M E L E K A T L E D L Q A K 321

978 CCG GTT GTT ATC AAC AAA GAT ACC ACC ACC ATC ATC GAT GGC GTG GGC GAC GAA GCT GCA ATC CAG GGT CCG GTG 1052
322 R V V I N K D T T T I I D G V G D E A A I Q G R V 346

1053 ACT CAG ATT CGT CAG CAG ATC GAA GAA GCA ACT TCC GAC TAT GAC CGT GAA AAA CTG CAG GAG CCG GTA GCG AAA 1127
347 T Q I R Q Q I E E A T S D Y D R E K L Q E R V A K 371

1128 CTG GCA GGC GGC GTT GCG GTT ATC AAA GTT GGT GCT GCG ACT GAA GTT GAA ATG AAA GAG AAG AAA GCC CCG GTT 1202
372 L A G G V A V I K V G A A T E V E M K E K K A R V 396

1203 GAA GAT GCG CTG CAC GCT ACC CGT GCT GCG GTA GAA GAA GGC GTG GTT GCT GGT GGT GCG GTT ATT CCG 1277
397 S D A L H A T R A A V E E G V V A G G V A L I R 421

1278 GTA GCG TCT AAA ATT GCG GCG CTG AAA GGT CAG AAC GAA GAC CAG AAC GTA GGT ATC AAA GTT GCG CTG CCG GCA 1352
422 V A S K I A G L K G Q N E D Q N V G I K V A L R A 446

1353 ATG GAA TCC CCA CTG CGT CAA ATC GTA CTG AAC TGC GGC GAA GAG CCG TCT GTA GTG GCT AAC ACC GTG AAA GCC 1427
447 M E S P L R Q I V L N C G E E P S V V A N T V K A 471

1428 GGT GAC GGT AAC TAC GGT TAC AAC GGT GCA ACT GAA GAA TAC GGC AAC ATG ATC GAC ATG GGT ATC CTG GAT CCA 1502
472 G D G N Y G Y N A A T E E Y G N M I D M G I L D P 496

1503 ACC AAA GTA ACT CGT TCT GCT CTG CAG TAC GCG GCT TCT GTT GCG GGT CTG ATG ATC ACC ACC GAG TGC ATG GGT 1577
497 T K V T R S A L Q Y A A S V A G L M I T T E C M V 521

1578 ACC GAC CTG CCG AAA GGC GAT GCA COT GAC TTA GGT GCT GCT GGT GGT ATG GGC GGC ATG GGC GGA ATG ATG TGA 1652
522 T D L P K G D A P D L G A A G G M G G M G G M M 546

1653 caagccgaattc 1665

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Figure 1

P65#44 -> Genes

DNA sequence 1654 b.p. gaattcggttcc ... aaagccgaattc linear

use to subclone for expression

P60-2

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1 gaattcggttccat ATG GCA AAA GAA ATT AAA TTT TCA TCA GAT GCC CGT TCA GCT ATG GTC CGT GGT GTC GAT ATC 77
1 M A K L I A S S D A R S A M V R G V D I 21

78 CTT GCA GAT ACT GTT AAA GTA ACT TTG GGA CCA AAA GGT CGC AAT GTC GTT CTT GAA AAG TCA TTC GGT TCA CCC 152
22 L A D T V K V T L G P K G R N V V L E K S F G S P 46

153 TTG ATT ACC AAT GAC GGT GTG ACT ATT GCC AAA GAA ATT GAA TTA GAA GAC CAT TTT GAA AAT ATG GGT GCC AAA 227
47 L I T N D G V T I A K E I E L E D H F E N M G A K 71

228 TTG GTA TCA GAA GTA GCT TCA AAA ACC AAT GAT ATC GCA GGT GAT GGA ACT ACA ACT GCA ACT GTT TTG ACC CAA 302
72 L V S E V A S K T N D I A G D G T T A T V L T Q 96

303 GCA ATC GTC CGT GAA GGA ATC AAA AAC GTC ACA GCA GGT GCA AAT CCA ATC GGT ATT CGT CGT GGG ATT GAA ACA 377
97 A I V R E G I K N V T A G A N P I G I R R G I E T 121

378 GCA GTT GCC GCA GCA GTT GAA GCT TTG AAA AAC AAC GTC ATC CCT GTT GCC AAT AAA GAA GCT ATC GCT CAA GTT 452
122 A V A A A V E A L K N N V I P V A N K E A I A Q V 146

453 GCA GCC GTA TCT TCT CGT TCT GAA AAA GTT GGT GAG TAC ATC TCT GAA GCA ATG GAA AAA GTT GGC AAA GAC GGT 527
147 A A V S S R S E K V G E Y I S E A M E K V G K D G 171

528 GTC ATC ACC ATC GAA GAG TCA CGT GGT ATG GAA ACA GAG CTT GAA GTC GTA GAA ATG CAG TTT GAC CGT GGT 602
172 V I T I E E S R G M E T E L E V V E G M Q F D R G 196

603 TAC CTT TCA CAG TAC ATG GTG ACA GAT AGC GAA AAA ATG GTG GCT GAC CTT GAA AAT CCG TAC ATT TTG ATT ACA 677
197 Y L S Q Y M V T D S E K M V A D L E N P Y I L I T 221

678 GAC AAG AAA ATT TCC AAT ATC CAA GAA ATC TTG CCA CTT TTG GAA AGC ATT CTC CAA AGC AAT CGT CCA CTC TTG 752
222 D K K I S N I Q E I L P L L E S I L Q S N R P L L 246

753 ATT ATT GCG GAT GAT GTG GAT GGT GAG GCT CTT CCA ACT CTT GTT TTG AAC AAG ATT CGT GGA ACC TTC AAC GTA 827
247 I I A D D V D G E A L P T L V L N K I R G T F N V 271

828 GTA GCA GTC AAG GCA CTT GGT TTT GGT GAC CGT CGC AAA GCC ATG CTT GAA GAT ATC GCC ATC TTA ACA GGC GGA 902
272 V A V K A P G F G D R R K A M L E D I A I L T G G 296

903 ACA GTT ATC ACA GAA GAC CTT GGT CTT GAG TTG AAA GAT GCG ACA ATT GAA GCT CTT GGT CAA GCA GCG AGA GTG 977
297 T V I T E D L G L E L K D A T I E A L G Q A A R V 321

978 ACC GTG GAC AAA GAT AGC ACG GTT ATT GTA GAA GGT GCA GGA AAT CCT GAA GCG ATT TCT CAC CGT GTT GCG GTT 1052
322 T V D K D S T V I V E G A G N P E A I S H R V A V 346

1053 ATC AAG TCT CAA ATC GAA ACT ACA ACT TCT GAA TTT GAC CGT GAA AAA TTG CAA GAA CGC TTG GCC AAA TTG TCA 1127
347 I K S Q I E T T T S E F D R E K L Q E R L A K L S 371

1128 GGT GGT GTA GCG GTT ATT AAG GTC GGA GCC GCA ACT GAA ACT GAG TTG AAA GAA ATG AAA CTC CGC ATT GAA GAT 1202
372 G G V A V I K V G A A T E T E L K E M K L R I E D 396

1203 GCC CTC AAC GGT ACT CGT GCA GGT GTT GAA GAA GGT ATT GTT GCA GGT GGT GGA ACA GCT CTT GCC AAT GTG ATT 1277
397 A L N A T R A A V E E G I V A G G G T A L A N V I 421

1278 CCA GCT GTT GCT ACC TTG GAA TTG ACA GGA GAT GAA GCA ACA GGA CGT AAT ATT GTT CTC CGT GCT TTG GAA GAA 1352
422 A V A T L E L T G D E A T G R N I V L R A L E E 446

1353 GGT GTT CTA ATT GCT CAC AAT GCA GGA TTT GAA GGA TCT ATC GTT ATC GAT CGT TTG AAA AAT GCT GAG CTT 1427
447 P V R Q I A H N A G F E G S I V I D R L K N A E L 471

1428 GGT ATA GGA TTC AAC GCA GCA ACT GGC GAG TGG GTT AAC ATG ATT GAT CAA GGT ATC ATT GAT CCA GTT AAA GTG 1502
472 G I G F N A A T G E W V N M I D Q G I I D P V K V 496

1503 AGT CGT TCA GCC GTA CAA AAT GCA GCA TCT GTA GCC AGC TTG ATT TTG ACA ACA GAA GCA GTC GTA GCC AAT AAA 1577
497 S R S A L Q N A A S V A S L I L T T E A V V A N K 521

1578 CCA GAA CCA GTA GCC CCA GCT CCA GCA ATG GAT CCA AGT ATG ATG GGT GGA ATG GGC GGA TGA aaagccgaattc 1654
522 P E P V A P A P A M D P S M H G G M G G 542

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Figure 2

Y65#5 -> Genes

DNA sequence 1662 b.p. gaattcggtttc ... caagtcgaattc linear

Y60-1

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1 gaattcggtttcat ATG GCG GCT AAA GAT GTA AAA TTC GGT AAC GAC GCT GGT GTA AAA ATG CTC CGC GGC GTA AAC 77
1 M A A K D V K F G N D A R V K M L R G V N 21

78 GTA CTG GCA GAC GCA GTT AAA GTA ACC CTG GCG CCG AAA GGC CGT AAC GTA GTG CTG GAC AAA TCC TTC GGC GCG 152
22 V L A D A Y K V T L G P K G R N V V L D K S F G A 46

153 CCA ACC ATC ACG AAA GAT GGT GTT TCT GTA GCA CGT GAA ATC GAG CTG GAA GAC AAG TTC GAA AAC ATG GGC GCG 227
47 P T I T K D G V S V A R E I E L E D K P E N M G A 71

228 CAG ATG GTG AAA GAA GTG GCC TCT AAA GCG AAC GAC GCT GCA GGC GAC GGT ACC ACC ACC GCG ACC GTG CTG GCT 302
72 Q M V K E V A S K A N D A A G D G T T A T V L A 96

303 CAG GCT ATC ATC ACC GAA GGT CTG AAA GCC GTT GCT GCG GGC ATG AAC CCA ATG GAT CTG AAA CGT GGT ATC GAC 377
97 Q A I I T E G L K A V A A G M N P M D L K R G I D 121

378 AAA GCT GTC GCG TCC GCT GTT GAA GAA CTG AAA GCG CTG TCC GTA CCG TGC TCT GAC TCT AAA GCC ATT GCT CAG 452
122 K A V A S A V E E L K A L S V P C S D S K A I A Q 146

453 GTA GGT ACC ATC TCC GCT AAC TCC GAC GAA ACC GTA GGT AAA CTG ATC GCG GAA GCG ATG GAT AAA GTC GGT AAA 527
147 V G T I S A N S D E T V G K L I A E A M D K V G K 171

528 GAA GGC GTT ATC ACC GTT GAA GAC GGT ACC GGT GGT GAA GAA GAA GAA GTG GTT GAA GGT ATG CAG TTC GAC 602
172 E G V I T V E D G T G L E D E L D V V E G M Q F D 196

603 CGC GGT TAC CTG TCC CCA TAC TTC ATC AAC AAG CCA GAA ACT GGC GCT GTT GAG CTG GAA AGC CCG TTC ATC CTG 677
197 R G Y L S P Y F I N K P E T G A V E L E S P F I L 221

678 CTG GCT GAC AAG AAA ATC TCC AAC ATC GCG GAA ATG CTG CCA GTG CTG GAA GCC GTT GCG AAA GCA GGC AAA CCG 752
222 L A D K K I S N I R E M L P V L E X V A K A G K P 246

753 CTG GTT ATC ATT GCT GAA GAC GTT GAA GCG GAA GCG CTG GCG ACC CTG GTG GTT AAC ACC ATG CGT GGC ATC GTG 827
247 L V I I A E D V E G E A L A T L V V N T M R G I V 271

828 AAA GTG GCT GCG GTT AAA GCA CCG GCG TTC GCG GAC GCG CGT AAA GCG ATG CTG CAG GAT ATC GCT ACC CTG ACC 902
272 K V A A V K A P G F G D R R K A M L Q D I A T L T 296

903 GGC GGT ACC GTC ATC TCT GAA GAG ATC GGT ATG GAG CTG GAA AAA GCG ACC CTG GAA GAC CTG GCG CAG GCT AAA 977
297 G G T V I S E E I G M E L E K A T L E D L G Q A K 321

978 CGT GTT GTG ATC AAC AAA GAC ACC ACC ACC ATC ATC GAT GGC GTG GGC GAC GAA GCG GCG ATT CAG GCG CGT GTT 1052
322 R V V I N K D T T T I I D G V G D E A A I Q G R V 346

1053 GGT CAG ATC CGT AAG CAG ATC GAA GAA GCC ACT TCC GAT TAC GAC CGT GAA AAA CTG CAG GAG CGC GTA GCG AAA 1127
347 G Q I R K Q I E E A T S D Y D R E K L Q E R V A K 371

1128 CTG GCA GGC GGT GTT GCG GTA ATC AAA GTC GGT GCT GCG ACT GAA GTT GAA ATG AAA GAG AAA AAA GCA GCG GTT 1202
372 L A G G V A V I K V G A A T E V E M K E K K A R V 396

1203 GAC GAT GCC CTG CAC GCG ACC CGT GCT GCG GTA GAA GAA GCG GTG GTT GCT GGT GGT GTG GCG CTG CTG CGT 1277
397 D D A L H A T R A A V E E G V V A G G G V A L V R 421

1278 GTT GCC GCG AAA CTG TCC GCG CTG ACT GCT CAG AAC GAA GAT CAG AAC GTG GGT ATC AAA GTT GCG CTG GCG GCA 1352
422 V A A K L S G L T A Q N E D Q N V G I K V A L R A 446

1353 ATG GAA GCT CCA CTG CGT CAG ATC GTG TCC AAC GCC GGT GAA GAG CCA TCT GTT GTG ACC AAC AAC GTG AAA GCA 1427
447 M E A P L R Q I V S N A G E E P S V V T N N V K A 471

1428 GGC GAA GGT AAC TAC GGT TAC AAC GCA GCA ACT GAA GAA TAC GGC AAC ATG ATC GAC TTC GGT ATC CTG GAT CCA 1502
472 G E G N Y G Y N A A T E E Y G N M I D F G I L D P 496

1503 ACC AAA GTG ACC CGT TCT GCT CTG CAG TAC GCG GCA TCT GTC GCT GCG CTG ATG ATC ACC ACC GAG TGC ATG GTG 1577
497 T K V T R S A L Q Y A A S V A G L M I T T E C M V 521

1578 ACC GAC CTG CCG AAA GCG GAC GCA CCG GAC TGA GGT GCT GCA GCG ATG GGT GCG ATG GCG GGT ATG ATG TGA caaa 1653
522 T D L P K G D A P D L G A A G M G G M J G M A 545

1654 gcggaattc 1662

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Figure 3

Y65#21 -> Genes

DNA sequence 1661 b.p. gaattcgggttc ... TAAGcgaattc linear

V261 - same in clone Y65#24, too
used to subclone for expression !!!

Y60-2

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1 gaattcgggttcgac atg gca aaa gaa atc aaa ttt tca gca gat ggc ggt gct gcc atg gtg cgc gga gtt gat atg 77
1 M A K E L R F S A D A R A A M V R G V D M 21

78 tta gca gat acc gtc aaa gta acg ctt ggt cct aaa ggg cgc aat gtt gtt ctt gaa aaa gct ttt ggt tct ccc 152
22 L A D T V K V T L G P K G R N V V L E K A F G S P 46

153 tta att act aat gac ggg gta acc att gct aaa gag atc gaa tta gaa gat cat ttt gaa aac atg gga gca aaa 227
47 L I T N D G V T I A K E I E L E D H F E N M G A K 71

228 ttg gtg tct gaa gtg gct tct aaa acc aat gat att gct ggt gat ggg acc act act gca aca gtt ttg aca caa 302
72 L V S E V A S K T N D I A G D G T T T A T V L T Q 96

303 gcc att gtt cat gaa gga cta aaa aat gtg aca gca ggt gct aat cca att ggt atc cgt cga gcc att gaa aca 377
97 A I V H E G L K N V T A G A N P I G I R R G I E T 121

378 gca aca gca aca gct gtt gaa gcc ttg aaa gcc att gct cca cct gta tct gcc aag gaa gct att gct cag gtc 452
122 A T A T A V E A L K A I A Q P V S G K E A I A Q V 146

453 gct gca gta tca tca cgc tct gaa aaa gtt gga gag tat atc tca gaa gct atg gag cgt gtg gcc aac gat ggt 527
147 A A V S S R S E K V G E Y I S E A M E R V G N D G 171

528 gtg att acc atc gaa gaa tct cga ggt atg gaa aca gaa ctt gaa gtg gtt gaa gcc atg caa ttt gac cgt ggt 602
172 V I T I E E S R G M E T E L E V V E G M Q F D R G 196

603 tac ctg tct caa tac atg gtc aca gac aat gaa aaa atg gtt gca gac ctt gaa aac cca ttt atc tta atc acc 677
197 Y L S Q Y M V T D N E K M V A D L E N P F I L I T 221

678 gat aaa aaa gtg tca aac atc caa gac att ttg cca cta ctt gag gaa gtt ctt aaa acc aac cgt cca tta ctc 752
222 D K K V S N I Q D I L P L L E E V L K T N R P L L 246

753 att att gca gat gat gtg gat ggt gaa gca ctt cca acc ctt gtc ttg aac aag att cgt ggt act ttc aat gtg 827
247 I I A D D V D G E A L P T L V L N K I R G T F N V 271

828 gtt gct gtc aaa gcc cca gga ttt ggt gat cgt cgt aaa gct atg ctt gaa gac att gct atc ttg aca ggt ggt 902
272 V A V K A P G F G D R R K A M L E D I A I L T G G 296

903 aca gtg att aca gag gat cta gga ctt gaa tta aaa gat gct aca atg aca gcc ctt gga cag gct gct aag att 977
297 T V I T E D L G L E L K D A T M T A L G Q A A K I 321

978 aca gtt gat aaa gat agc aca gta att gtt gaa ggt tca gga agt tca gaa gct att gct aac cgt att gca ctg 1052
322 T V D K D S T V I V E G S G S S E A I A N R I A L 346

1053 att aaa tgg caa tta gaa aca aca act tct gac ttt gac cgt gaa aaa cta caa gaa cgt ttg gcc aaa tta gct 1127
347 I K S Q L E T T T S D F D R E K L Q E R L A K L A 371

1128 ggt ggt gta gct gtt atc aaa gta gga gct cca aca gag aca gct tta aaa gaa atg aaa ctt cgc att gag gat 1202
372 G G V A V I K V G A P T E T A L K E M K L R I E D 396

1203 gct cta aat gct aca cgt gca gcc gtt gaa gaa ggt atc gtt gct ggt ggt gga aca gca ctt att acc gtt att 1277
397 A L N A T R A A V E E G I V A G G G T A L I T V I 421

1278 gaa aaa gta gca gct ctt gag ctt gag gcc gat gat gct act gga cgt aac att gtg ctt cgt gct cta gaa gag 1352
422 E K V A A L E L E G D D A T G R N I V L R A L E E 446

1353 ctt gta cgt caa att gct tta aat gct ggg tac gaa gcc tcc gta gtt att gac aag ttg aaa aac acc cgt gca 1427
447 P V R Q I A L N A G Y E G S V V I D K L K N S P A 471

1428 gga aca gga ttt aat gct gca aca ggt gag tgg gtt gat atg att aaa aca gga atc att gac cgt gtc aaa gta 1502
472 G T G F N A A T G E W V D M I K T G I I D P V K V 496

1503 aca cga tca gcc ctt cca aat gca gct tct gta gct agt ctt att ttg aca aca gaa gca gtt gtt gct aat aaa 1577
497 T R S A L Q N A A S V A S L I L T T E A V V A N K 521

1578 cct gaa cca gct acc cca gcc cca gca atg cca gca ggt atg gat cca gga atg atg ggt ggc atg gcc gga tta 1652
522 P E P A T P A P A M P A G M D P G M N G G M G J 546
1653 ggcgaattc 1661

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Figure 4

Sequencing strategy (scale : 1cm = approx. 100bp)

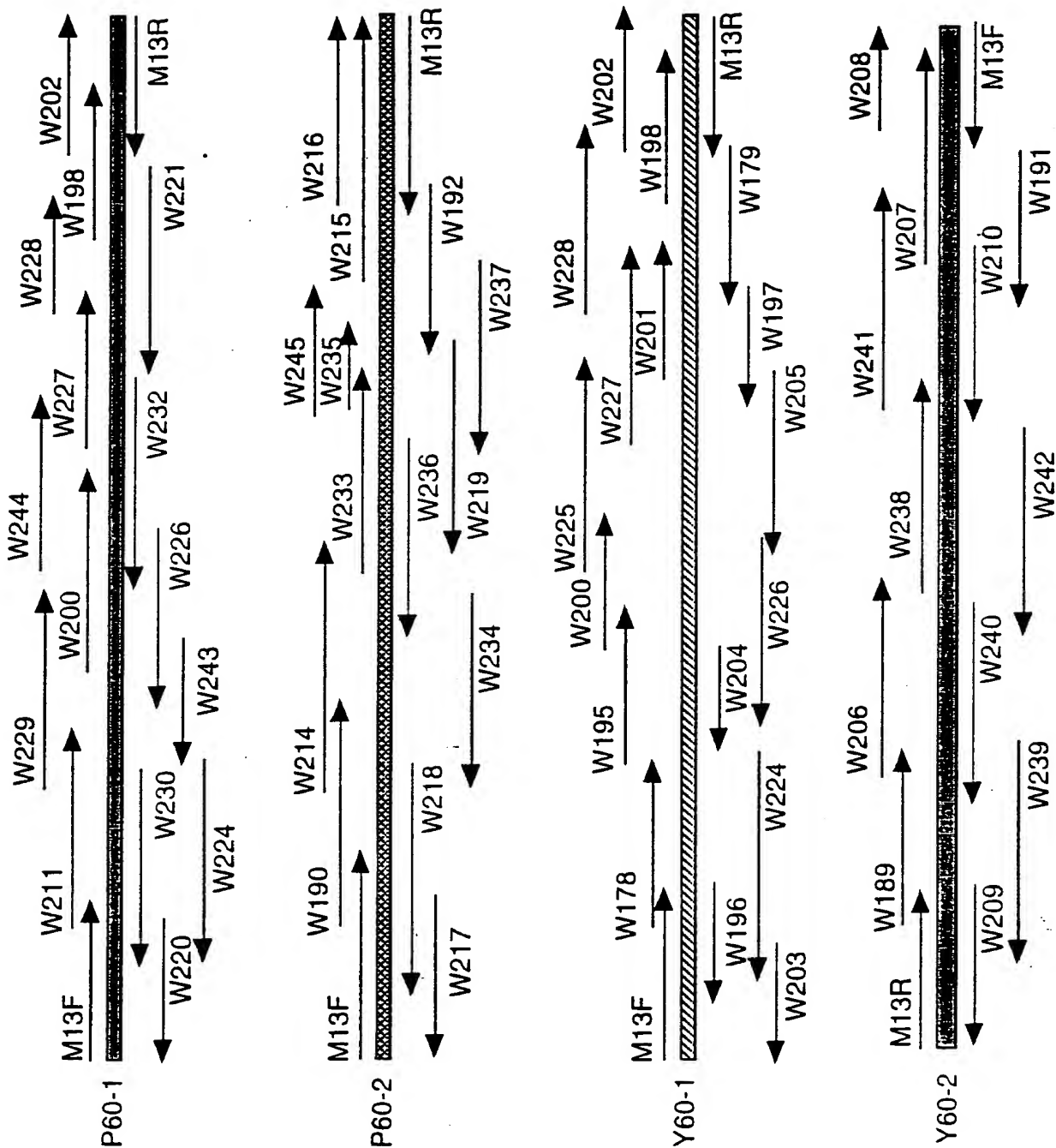


Figure 5

T7 expression construct of His-tagged *Streptococcus pneumoniae* hsp60-1
 PCR product starts at NdeI (58) site and ends at EcoRI site (1706)

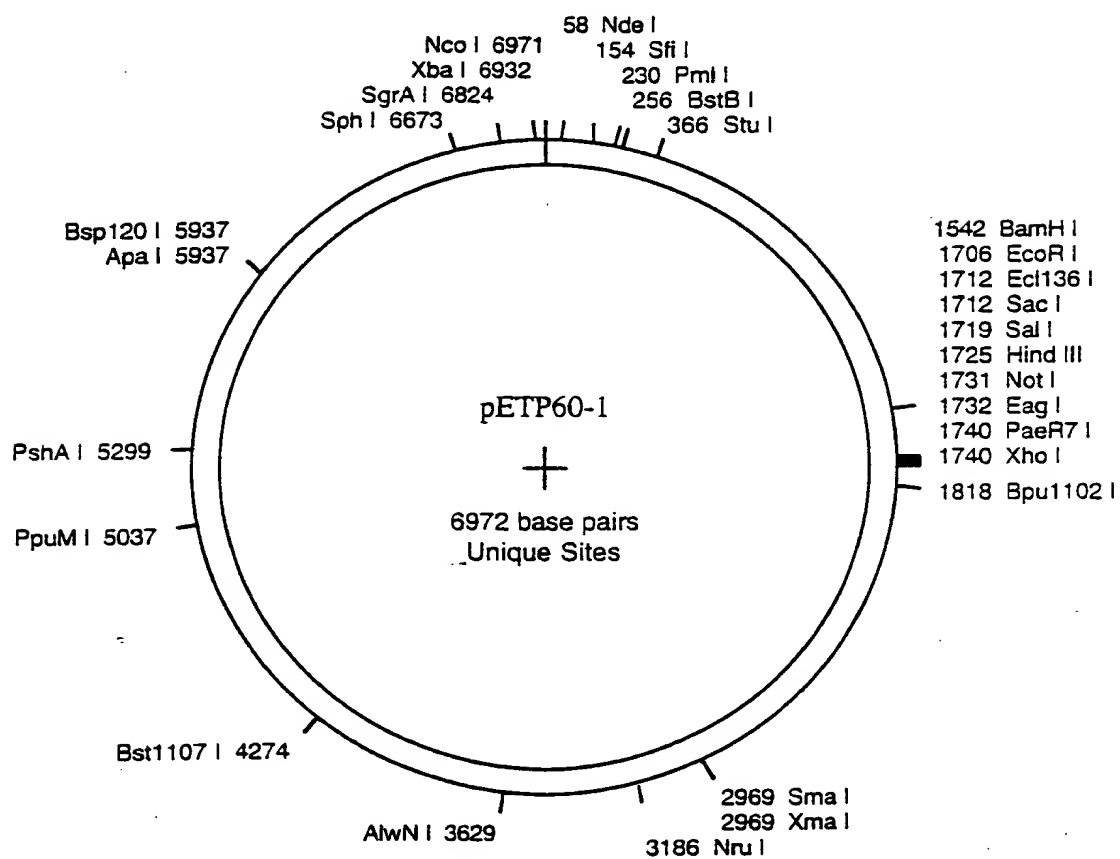


Figure 6

T7 expression construct of His-tagged *Streptococcus pneumoniae* hsp60-2
 PCR product starts at NdeI (58) site and ends at EcoRI site (1695)

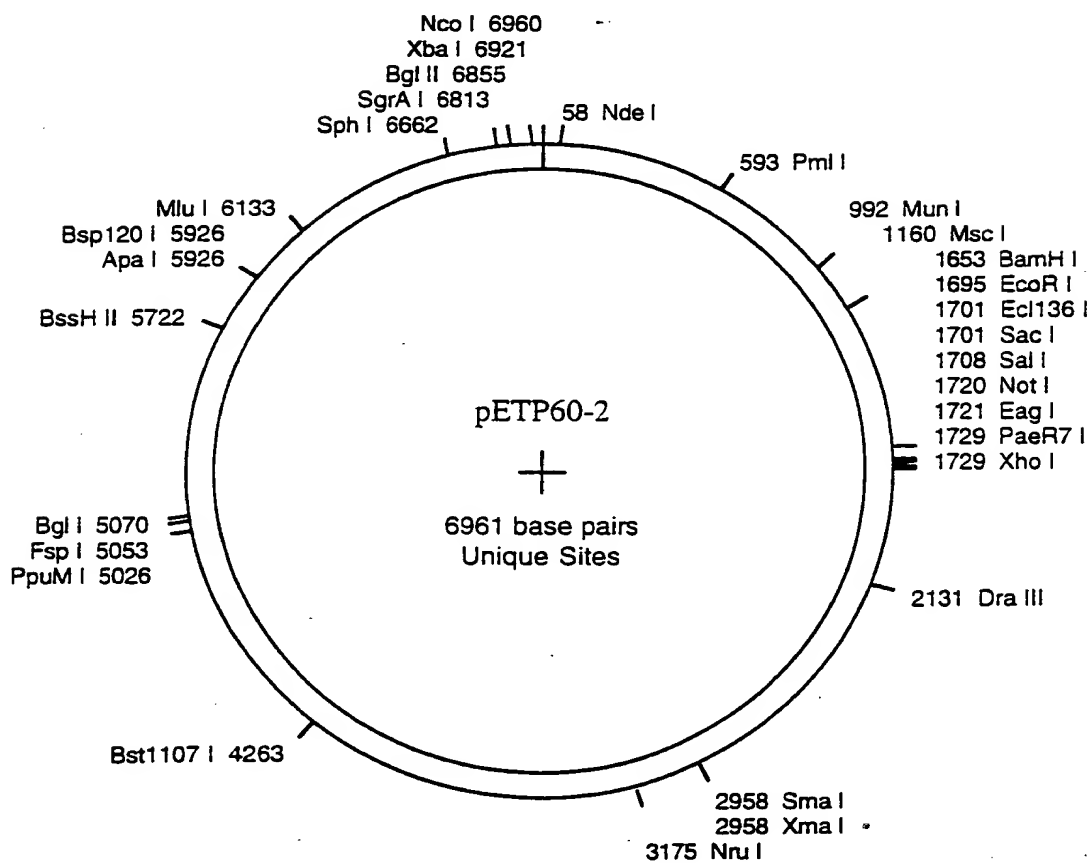


Figure 7

T7 expression construct of His-tagged *Streptococcus pyogenes* hsp60-1
 PCR product starts at NdeI (58) site and ends at EcoRI site (1703)

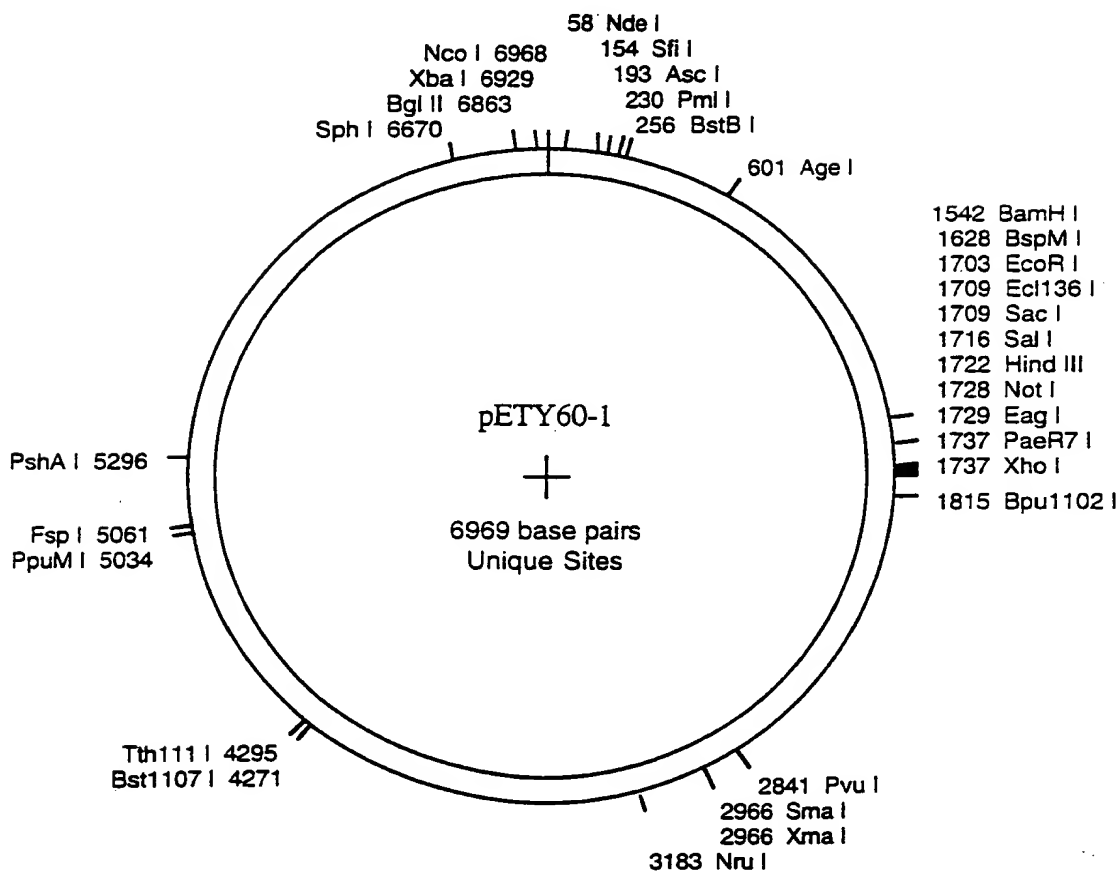


Figure 8

T7 expression construct of His-tagged *Streptococcus pyogenes* hsp60-2
 PCR product starts at NdeI (58) site and ends at EcoRI site (1702)

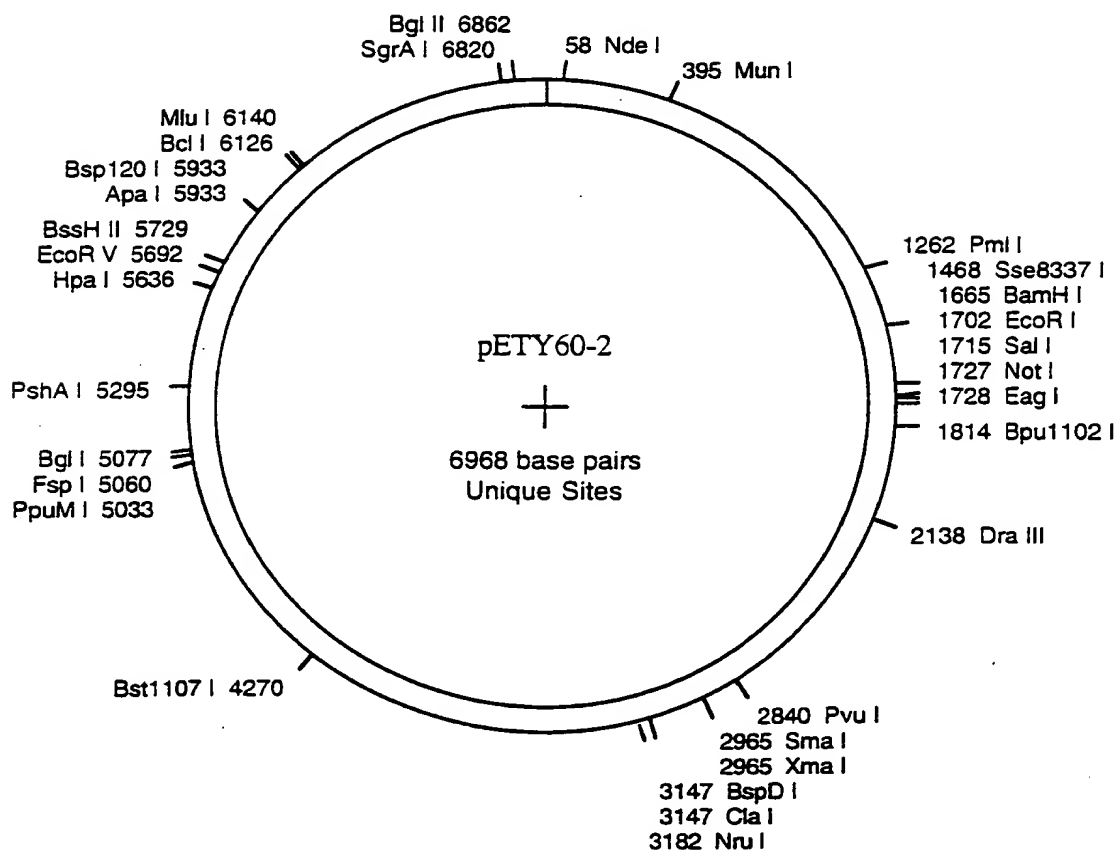


Figure 9

MA	10	20	30	40	50	60	70	80	90	100	110	120	130
S. pneumoniae MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
S. pyogenes hs MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
S. pneumoniae MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
S. pyogenes hs MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
B. subtilis gr MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Clostridium h MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Cowdria hsp60 MANN	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Haemophilus h MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
L. pneumophila MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
M. avium hsp60 MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
M. bovis hsp60 MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
M. leprae groE HS	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
M. leprae hsp6 MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
M. tuberculosis HS	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
N. meningitidis MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
S. aureus hsp6 MV	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Synechocystis HS	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Synechocystis HS	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Tsukamurella MA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
S. pombe hsp60 M	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
S. cerevisiae M	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
P. falciparum M	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Onchocerca hs MTNV	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
C. elegans hsp M	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
D. melanogaster H	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
human hsp60 M	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Arabidopsis h M	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
maize hsp60 M	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
RUBISCO chape	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Figure 10A

AGDGTITATVLAQAIKVRKGLKVAAGANPMDLRGIDKAVDAVVEELKAIKAPV--ETKEEIAQVATISANDEEIGE---	140	150	160	170	180	190	200	210	220	230	240	250	260
S.pneumoniae	AGDGTITATVLAQSIITEGLKAVAAAGNPNMDLKRIGDKAVAAAVEELKALSVFC--SDSKAIAQVGTISANSDETGVK---												
S.pyogenes hs	AGDGTITATVLAQAIITEGLKAVAAAGNPNMDLKRIGDKAVASAVEELKALSVFC--SDSKAIAQVGTISANSDETGVK---												
S.pneumoniae	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKNNVTPV--ANKKEIAQVAVSS--RSEKVE---												
S.pyogenes hs	AGDGTITATVLAQAIIVHGLKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
B.subtilis gr	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
Clostridium h	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
Haemophilus h	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
L.pneumophila	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
M.avium hsp60	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
M.bovis hsp60	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
M.leprae groE	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
M.leprae hsp6	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
M.tuberculosis	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
N.meningitidis	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
S.aureus hsp6	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
Synechocystis	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
Synechocystis	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
Tsukamurella	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
S.pombe hsp60	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
S.cerevisiae	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
P.falciparum	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
Onchocerca hs	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
C.elegans	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
D.melanogaste	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
human hsp60	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
Arabidopsis h	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
maize hsp60	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												
RUBISCO chape	AGDGTITATVLAQAIIVREGIKNVTAGANPIGIRRGIEITAVAAAVEALKAIKAPV--SGKEAJAQAVALSS--RSEKVE---												

Figure 10B

S. pneumoniae NRPETGAVELSPFILLADKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 S. pyogenes hs NRPETGAVELSPFILLADKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 S. pneumoniae TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 S. pyogenes hs TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 B. subtilis gr TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 Clostridium h TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 Cowdria hsp60 TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 Haemophilus h NRPETGAVELSPFILLADKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 L. pneumophila NRPETGAVELSPFILLADKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 M. avium hsp60 TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 M. bovis hsp60 TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 M. leprae groE TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 M. tuberculosis h TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 N. meningitidis h TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 S. aureus hsp60 TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 Synchocystis h TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 Synechocystis h TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 Tsukamurella h TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 S. pombe hsp60 TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 S. cerevisiae h TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 P. falciparum h TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 Onchocerca h TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 C. elegans hsp TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 D. melanogaster h TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 human hsp60 TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 Arabidopsis h TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 maize hsp60 TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331
 RUBISCO chape TDSKQVADLENPFIITDKKISNIREMLPVEAVA--KAGKPLIIIAEDVEGEALATLVNTHIRGIVKVAAPGFGDRRKAMLDIAITLGGTIVSEE--IGMELEKATLED--LGOAKRVVINKDITTT 331

Figure 10C

	400	410	420	430	440	450	460	470	480	490	500	510	520
IUDGAGD--	AAIAGRAVQIRSQIEEST--SDYDKEKLOERLAKLAGGVAVIKVGAATEVELKERKDRVEDALANTRAABEGIVPGGGVALLRAAPALDKLKE--NGDEATGNIVILRALEAPLROIAE												
S. pneumoniae	IIDGVGD--EAAIQRVTOIRQIEEAT--SDYDREKLOERVAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVASKIAGIKGQ--NEDQNVGIKVALRAMESPLROIVL												456
S. pyogenes hsp	IIDGVGD--EAAIQRVGOIRKQIEEAT--SDYDREKLOERVAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												456
S. pneumoniae	IVBAGN--FENAIHRAVAVIKSQIETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												453
S. pyogenes hsp	IVBAGN--FENAIHRAVAVIKSQIETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												453
B. subtilis gr	IVBAGE--TUKISARVTOIRQIEEAT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												453
Clostridium h	IVNGRN--SEFIKNRINQIKQIEEAT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												453
Cowdria hsp60	II--GSUNSCNIVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												454
Haemophilus h	IIDGEG--FAOIQRVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												458
L. pneumophila	IIDGEG--ATEINARITQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												455
M. avium hsp60	IVBAGD--SDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												455
M. bovis hsp60	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												453
M. leprae groE	IVDGGG--SDAVANRAKILRAEIDKSD--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												453
M. leprae hsp60	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												455
M. tuberculosis	IIDGEG--TAEVANRAKILRAEIDKSD--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												453
M. tuberculosis	IIDGEG--TAEVANRAKILRAEIDKSD--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												453
S. aureus hsp60	IVDGGG--TAEVANRAKILRAEIDKSD--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												456
Synechocystis	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												456
Synechocystis	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												456
Tsukamurella	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												454
S. pombe hsp60	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												458
S. cerevisiae	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												452
P. falciparum	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												478
Onchocerca hsp	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												483
C. elegans hsp	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												472
D. melanogaster	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												481
human hsp60	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												481
Arabidopsis hsp60	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												486
maize hsp60	IVBAGD--TDAIAGRAVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												489
RUBISCO chape	ITADAASK--DELQSRVQAKKELSETD--SIYDSEKLAERIAKLSGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGGVALIRVAKUSGLUQ--NEDQNVGIKVALRAMESPLROIVS												503

Figure 10D

	530	540	550	560	570	580	590	600	610	620
NAGLEGSV-VVEKVN	---	SEAG-GYNAATGEVVDIAAGIIDPTKVT	SALQNAASVASILMTTTEAVVDKPEKAPAG-MFGM	---	MCGMGCMGM	---	M			
S.pneumoniae	NCGEFSPV-VNTTVKA	---	GDGNGYGYNAATEEYGNMIDGILDFTKV	TSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
S.pyogenes hs	NAGEFSPV-VNTTVKA	---	GBGNGYGYNAATEEYGNMIDGILDFTKV	TSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
S.pneumoniae	NAGFSGI-VIDRLKN	---	ABLGLGFNAATGEWMNIDQGLIDPQKVS	RALQNAASVASILMTTEAVVANKPEFVAPAPA-M	---	DPNMCMGCG				
S.pyogenes hs	NAGLEGSV-VIDRLKN	---	SPAGTGFNAATGEWMNIDQGLIDPQKVS	RALQNAASVASILMTTEAVVANKPEFVAPAPA-M	---	DPNMCMGCG				
B.subtilis gr	NAGLEGSV-IVERLKN	---	BEIGVGFNAAATGEWMNIEKGLIDPQKVS	RALQNAASVASILMTTEAVVANKPEFVAPAPA-M	---	DPNMCMGCG				
Clostridium h	NAGLEGSV-IIEKVN	---	SDAGVGFDALRGGEWMNIEKGLIDPQKVS	RALQNAASVASILMTTEAVVANKPEFVAPAPA-M	---	DPNMCMGCG				
Cowdria hsp60	NAGSENAFCVIAHLKQNDKELI	---	FNVDVTFNFAATFTSGVIDPLKVVRIAF	DFNSLAASVETILNNUVDIPSKDINS	AAGNGMGCMGCG					
Haemophilus h	NAGEASV-IASAVKN	---	GBGNGFYNAATGEYGDMLANGILDFTKV	TSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
L.pneumophila	NAGEASV-VNKNVAE	---	HKDNVGYNAATGEYGDMLANGILDFTKV	TSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
M.avium hsp60	NGGLERG-VAEKVN	---	SPAGTGLANAATGEYEDLLKAGIADPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
M.bovis hsp60	NSGLEFV-VAEKVN	---	LPAGHGLAATQGVYEDLLAAGVADPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
M.leprae groB	NAGLDAN-VVDKVG	---	LPAGHGLAATQGVYEDLLAAGVADPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
M.leprae hsp6	NSGMERG-VAEKVN	---	LSVGHGLAATQGVYEDLLAAGVADPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
M.tuberculosis	NAGLDGV-VVKVSE	---	LPAGHGLAATQGVYEDLLAAGVADPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
N.meningitidis	NAGLEGSV-VNKNVAE	---	KGNVGYNAATGEYGDMLANGILDFTKV	TSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
S.aureus hsp6	NAGLEGSV-IVERLKN	---	AEPGVGFGNATGEWMNIDQGLIDPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
Synechocystis	NAGQNGA-IVERLKN	---	KEFNVGYNAATGEYGDMLANGILDFTKV	TSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
Synechocystis	NAGLEGSV-IVERLKN	---	ATNGQNGVNVITGKIEDLJAAGIIDPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
Tsakumarella	NAGLEGSV-VAEKVN	---	SPAGTGLANAATGEYEDLLAAGVADPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
S.pombe hsp60	NAGLEGNL-IVGKLKELVGEFNI	---	GYDIAKDFPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
S.cerevisiae	NAGEGSV-IIGKLDIYEDGDF	---	AKGYDASKEYSYDMLATGIDPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
P.falciparum	NAGHESV-VAGNLIKDKNSNI	---	GFNAQGEYKVDNIESGIIIDPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
Onchocerca hs	NAGLESV-IIDYLIKQNNKELI	---	VNVEAMSYANFAAGVIDPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
C.elegans hsp	NAGLEPSS-IIDEVGTNSVTS	---	GYDALMGKFVDMFEAGIIDPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
D.melanogaste	NAGVGNM-VAKVENQAG-DY	---	GYDA-KGEYGNLIEKGIIDPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
human hsp60	NAGVEGSL-IVEKIM-QSSSEV	---	GYDAMAGDFVNVKEGIIIDPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
Arabidopsis h	NAGVEGAV-IVGKLLEQNPDL	---	GYDAAKGEYDMVKAGIIDPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
malze hsp60	NAGVEGAV-IVGKLLEQNPDL	---	GYDAAKGEYDMVKAGIIDPQKVS	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				
RUBISCO chape	NAGIB3EV-VVEKLN	---	GBEYGVNATVITYENLVESGVIDPAKVT	RALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG	---	MGCMGCG				

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Current Chromatogram(s)

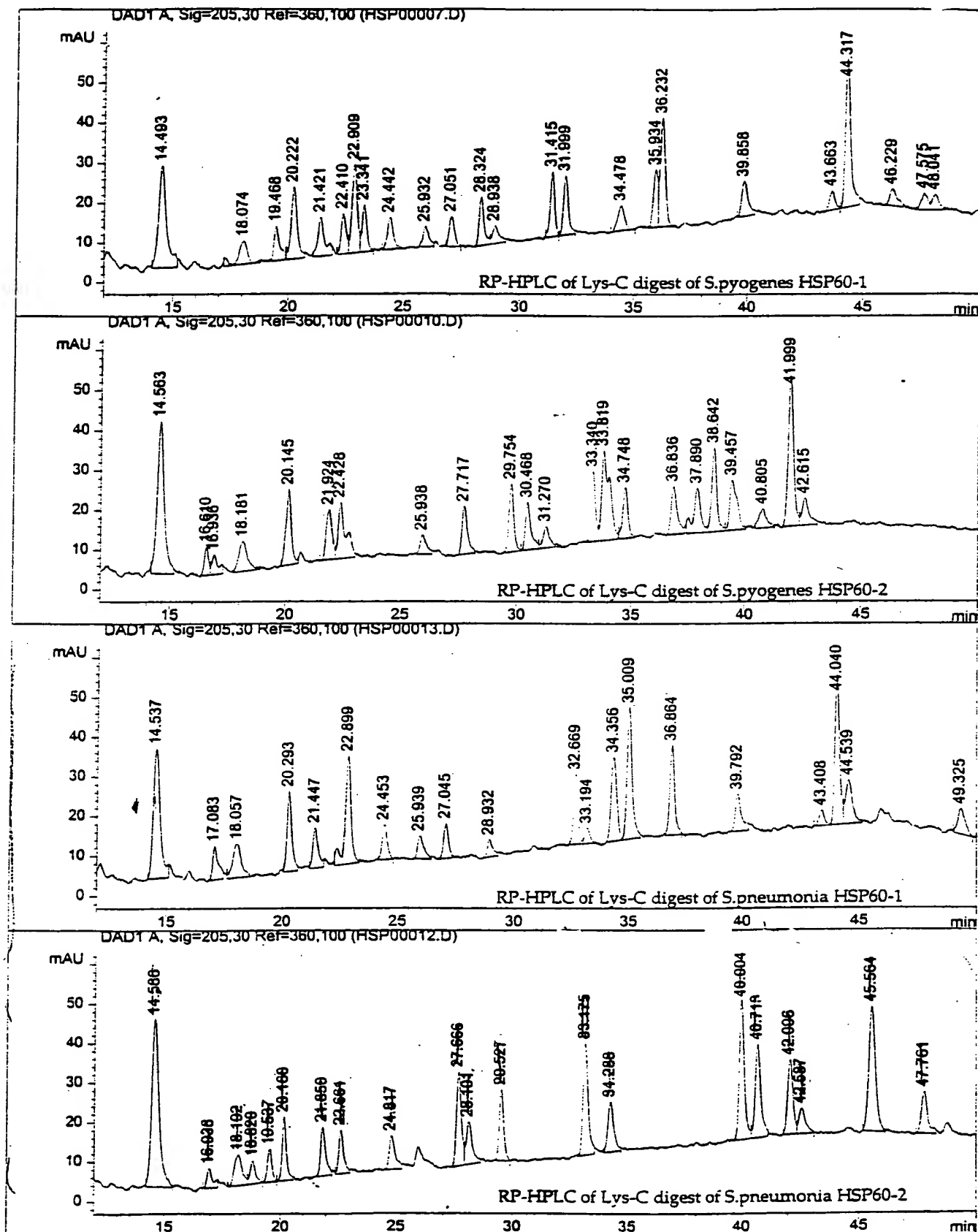


Figure 11